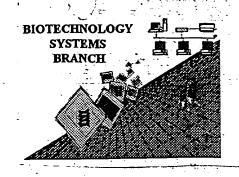BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/606,129_

Source: _OIPE_

Date Processed by STIC: _7/12/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

OIPE

```
            RAW SEQUENCE LISTING                  DATE: 07/12/2000
            PATENT APPLICATION:   US/09/606,129    TIME: 10:58:14

            Input Set : A:\U607921.app
            Output Set: N:\CRF3\07122000\I606129.raw
```

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      3 <110> APPLICANT: Maines, Mahin D.
      5 <120> TITLE OF INVENTION: BILIVERDIN REDUCTASE FRAGMENTS AND VARIANTS, AND
      6        METHODS OF USING BILIVERDIN REDUCTASE AND SUCH
      7        FRAGMENTS AND VARIANTS
      9 <130> FILE REFERENCE: 176/60792
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/606,129
C--> 12 <141> CURRENT FILING DATE: 2000-06-28
     14 <150> PRIOR APPLICATION NUMBER: 60/141,309
     15 <151> PRIOR FILING DATE: 1999-06-28
     17 <150> PRIOR APPLICATION NUMBER: 60/163,223
     18 <151> PRIOR FILING DATE: 1999-11-03
     20 <160> NUMBER OF SEQ ID NOS: 37
     22 <170> SOFTWARE: PatentIn Ver. 2.1
     24 <210> SEQ ID NO: 1
     25 <211> LENGTH: 296
     26 <212> TYPE: PRT
     27 <213> ORGANISM: Homo sapiens
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     31  1               5                  10                  15
     33 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
     34              20                  25                  30
     36 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
     37          35                  40                  45
     39 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
     40      50                  55                  60
     42 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
     43  65                  70      ·          75                  80
     45 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
     46                  85                  90                  95
     48 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
     49              100                 105                 110
     51 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
     52          115                 120                 125
     54 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
     55      130                 135                 140
     57 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp
     58 145                 150                 155                 160
     60 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
     61              165                 170                 175
     63 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
     64          180                 185                 190
     66 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
     67          195                 200                 205
     69 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
     70      210                 215                 220
     72 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
```

see

p.5

RAW SEQUENCE LISTING   DATE: 07/12/2000
PATENT APPLICATION: US/09/606,129   TIME: 10:58:14

Input Set : A:\U607921.app
Output Set: N:\CRF3\07122000\I606129.raw

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73 225                  230                  235                  240
75 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
76              245                  250                  255
78 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
79              260                  265                  270
81 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
82         275                  .  280                  285
84 Gln Lys Tyr Cys Cys Ser Arg Lys
85      290                  295
88 <210> SEQ ID NO: 2
89 <211> LENGTH: 1070
90 <212> TYPE: DNA
91 <213> ORGANISM: Homo sapiens
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94  ggggtggcgc ccggagctgc acggagagcg tgcccgtcag tgaccgaaga agagaccaag 60
95  atgaatgcag agcccgagag gaagtttggc gtggtgttgg ttggtgttgg ccgagccggc 120
96  tccgtgcgga tgagggactt gcggaatcca caccctcct cagcgttcct gaacctgatt 180
97  ggcttcgtgt cgagaaggga gctcgggagc attgatggag tccagcagat ttctttggag 240
98  gatgctcttt ccagccaaga ggtggaggtc gcctatatct gcagtgagag ctccagccat 300
99  gaggactaca tcaggcagtt ccttaatgct ggcaagcacg tccttgtgga atacccatg 360
100 acactgtcat tggcggccgc tcaggaactg tgggagctgg ctgagcagaa aggaaaagtc 420
101 ttgcacgagg agcatgttga actcttgatg gaggaattcg ctttcctgaa aaaagaagtg 480
102 gtggggaaag acctgctgaa agggtcgctc ctcttcacat ctgacccgtt ggaagaagac 540
103 cggtttggct tccctgcatt cagcggcatc tctcgactga cctggctggt ctccctcttt 600
104 ggggagcttt ctcttgtgtc tgccactttg gaagagcgaa aggaagatca gtatatgaaa 660
105 atgacagtgt gtctggagac agagaagaaa agtccactgt catggattga agaaaaagga 720
106 cctggtctaa aacgaaacag atatttaagc ttccatttca agtctgggtc cttggagaat 780
107 gtgccaaatg taggagtgaa taagaacata tttctgaaag atcaaaatat atttgtccag 840
108 aaactcttgg gccagttctc tgagaaggaa ctggctgctg aaaagaaacg catcctgcac 900
109 tgcctggggc ttgcagaaga aatccagaaa tattgctgtt caaggaagta agaggaggag 960
110 gtgatgtagc acttccaaga tggcaccagc atttggttct tctcaagagt tgaccattat 1020
111 ctctattctt aaaattaaac atgttgggga aacaaaaaaa aaaaaaaaa          1070
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 296
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 3
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121 1                   5                   10                  15
123 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
124              20                  25                  30
126 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
127         35                  40                  45
129 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
130      50                  55                  60
132 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
133 65                  70                  75                  80
135 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
136              85                  .   90                  95
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Input Set : A:\U607921.app
Output Set: N:\CRF3\07122000\I606129.raw

```
138 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
139             100                 105                 110
141 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
142         115                 120                 125
144 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
145     130                 135                 140
147 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
148 145             ,   150                 155                 160
150 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
151             165                 170                 175
153 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
154         180             .   185                 190
156 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
157         195                 200                 205
159 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
160         210                 215                 220
162 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
163 225                 230                 235                 240
165 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
166             245                 250                 255
168 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
169             260                 265                 270
171 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
172         275                 280                 285
174 Gln Lys Tyr Cys Cys Ser Arg Lys
175     290                 295
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 295
180 <212> TYPE: PRT
181 <213> ORGANISM: Rattus norvegicus
183 <400> SEQUENCE: 4
184 Met Asp Ala Glu Pro Lys Arg Lys Phe Gly Val Val Val Gly Val
185   1                 5                   10                  15
187 Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
188             20                  25                  30
190 Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
191         35                  40                  45
193 Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
194     50                  55                  60
196 Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu
197 65                  70                  75                  80
199 Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu
200             85                  90                  95
202 Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu
203             100                 105                 110
205 Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu
206         115                 120                 125
208 Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu
209     130                 135                 140
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211 Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg
212 145                 150                 155                 160
214 Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val
215             165                 170                 175
217 Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg
218             180                 185                 190
220 Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn
221         195                 200                 205
223 Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg
224     210                 215                 220
226 Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val
227 225                 230                 235                 240
229 Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile
230             245                 250                 255
232 Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala
233         260                 265                 270
235 Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln
236         275                 280                 285
238 Lys Leu Cys His Gln Lys Lys
239     290                 295
242 <210> SEQ ID NO: 5
243 <211> LENGTH: 1081
244 <212> TYPE: DNA
245 <213> ORGANISM: Rattus norvegicus
247 <400> SEQUENCE: 5
248 ggtcaacagc taagtgaagc catatccata gagagtttgt gccagtgccc caagatcctg 60
249 aacctctgtc tgtcttcgga cactgactga agagaccgag atggatgccg agccaaagag 120
250 gaaatttgga gtggtagtgg ttggtgttgg cagagctggc tcggtgaggc tgagggactt 180
251 gaaggatcca cgctctgcag cattcctgaa cctgattgga tttgtgtcca gacgagagct 240
252 tgggagcctt gatgaagtac ggcagatttc tttgtgaagat gctctccgaa gccaagagat 300
253 tgatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagtttct 360
254 gcaggctggc aagcatgtcc tcgtggaata ccccatgaca ctgtcatttg cggcggccca 420
255 ggagctgtgg gagctggccg cacagaaagg gagagtcctg catgaggagc acgtggaact 480
256 cttgatggag gaattcgaat tcctgagaag agaagtgttg gggaaagagc tactgaaagg 540
257 gtctcttcgc ttcacagcta gcccactgga agaagagaga tttggcttcc ctgcgttcag 600
258 cggcatttct cgcctgacct ggctggtctc cctcttcggg gagctttctc ttatttctgc 660
259 caccttggaa gagcgaaaag aggatcagta tatgaaaatg accgtgcagc tggagaccca 720
260 gaacaagggt ctgctgtcat ggattgaaga gaaagggcct ggcttaaaaa gaaacagata 780
261 tgtaaacttc cagttcactt ctgggtccct ggaggaagtg ccaagtgtag gggtcaataa 840
262 gaacattttc ctgaaagatc aggatatatt tgttcagaag ctcttagacc aggtctctgc 900
263 agaggacctg gctgctgaga agaagcgcat catgcattgc ctggggctgg ccagcgacat 960
264 ccagaagctt tgccaccaga agaagtgaag aggaagcttc agagacttct gaagggggcc 1020
265 agggtttggt cctatcaacc attcacctttt agctcttaca attaaacatg tcagataaac 1080
266 a                                                                  1081
269 <210> SEQ ID NO: 6
270 <211> LENGTH: 6
271 <212> TYPE: PRT
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
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        RAW SEQUENCE LISTING                       DATE: 07/12/2000
        PATENT APPLICATION:  US/09/606,129         TIME: 10:58:14

        Input Set : A:\U607921.app
        Output Set: N:\CRF3\07122000\I606129.raw

275 <223> OTHER INFORMATION: Description of Artificial Sequence: hydrophobic
276       domain of BVR
278 <220> FEATURE:
279 <221> NAME/KEY: PEPTIDE
280 <222> LOCATION: (2)
281 <223> OTHER INFORMATION: where X is any aa
283 <400> SEQUENCE: 6
284 Phe Xaa Val Val Val Val
285   1           5
288 <210> SEQ ID NO: 7
289 <211> LENGTH: 6
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
295       binding domain of BVR
297 <220> FEATURE:
298 <221> NAME/KEY: PEPTIDE
299 <222> LOCATION: (2)
300 <223> OTHER INFORMATION: where X is any aa
302 <400> SEQUENCE: 7
303 Gly Xaa Gly Xaa Xaa Gly
304   1           5
307 <210> SEQ ID NO: 8
308 <211> LENGTH: 8
309 <212> TYPE: PRT
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Description of Artificial Sequence:
314       oxidoreductase domain of BVR
316 <400> SEQUENCE: 8
317 Ala Gly Leu His Val Leu Val Glu
318   1           5
321 <210> SEQ ID NO: 9
322 <211> LENGTH: 29
323 <212> TYPE: PRT
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence: leucine
328       zipper of BVR
330 <220> FEATURE:
331 <221> NAME/KEY: PEPTIDE
332 <222> LOCATION: (2)
333 <223> OTHER INFORMATION: where X is any aa
335 <400> SEQUENCE: 9
336 Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa
337   1           5               10              15
339 Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu
340         20               25
```

(handwritten annotation): ← what about Xaa's at location 3-7, 9-14, 16-21, 23-28 ?

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 07/12/2000
PATENT APPLICATION: US/09/606,129   TIME: 10:58:15

Input Set : A:\U607921.app
Output Set: N:\CRF3\07122000\I606129.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6·
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17